

SEQUENCE LISTING

<110> MENZEL, ROLF

<120> COMPOSITIONS AND METHODS FOR DIRECTED GENE ASSEMBLY

<130> 10424-003

<150> 60/222,134

<151> 2000-07-31

<160> 22

<170> PatentIn version 3.0

<210> 1

<211> 87

<212> DNA

<213> Artificial

<220>

<223> Description of artificial sequence: Primer

<400> 1

aattcgcggtt taaacttaat taaggtagcc attttttggc agatctagac caaaaaatgg 60
gggcggccgc tccccgggtg gcgcgcc 87

<210> 2

<211> 87

<212> DNA

<213> Artificial

<220>

<223> Description of artificial sequence: Primer

<400> 2

aattggcgcg ccacccgggg agcggccgcc cccatttttt ggtctagatc tgccaaaaaa 60
tgggtacctt aattaagttt aaacgcg 87

<210> 3

<211> 50

<212> DNA

<213> Artificial

<220>

<223> Description of artificial sequence: Primer

<400> 3

gactgcgaga tcatagatat agatttcact acgcggctgc tcaaacctgg 50

<210> 4

<211> 50

<212> DNA

<213> Artificial

<220>

<223> Description of artificial sequence: Primer

<400> 4
 ccaggtttga gcagccgcgt agtgaaatct atatctatga tctcgcatc 50

<210> 5
 <211> 87
 <212> DNA
 <213> Artificial

<220>
 <223> Description of artificial sequence: Primer

<400> 5
 aatttaccat ggagcaattg catatgggtt aaacagctcg agtagatctt gcggccgctt 60
 ggctagcgtc agctgggtac catgcat 87

<210> 6
 <211> 87
 <212> DNA
 <213> Artificial

<220>
 <223> Description of artificial sequence: Primer

<400> 6
 cgcgttatgc atggtaccca gctgacgcta gccaaagcggc cgcaagatct actcgagctg 60
 tttaaaccat atgcaattgc tccatgg 87

<210> 7
 <211> 19
 <212> DNA
 <213> Artificial

<220>
 <223> Description of artificial sequence: Primer

<400> 7
 cgcaawcygt tccttaygg 19

<210> 8
 <211> 20
 <212> DNA
 <213> Artificial

<220>
 <223> Description of artificial sequence: Primer

<400> 8
 gccaggagcc atsacwtcaa 20

<210> 9
 <211> 28
 <212> DNA
 <213> Artificial

<220>
 <223> Description of artificial sequence: Primer

<400> 9

ggggtaccgc ggtctattca tactttcg 28

<210> 10
 <211> 36
 <212> DNA
 <213> Artificial

<220>
 <223> Description of artificial sequence: Primer

<400> 10
 gcagatctca tttgtttagaa tatggtattg agcggc 36

<210> 11
 <211> 27
 <212> DNA
 <213> Artificial

<220>
 <223> Description of artificial sequence: Primer

<400> 11
 agcgagatct ctattattgt gcagctg 27

<210> 12
 <211> 33
 <212> DNA
 <213> Artificial

<220>
 <223> Description of artificial sequence: Primer

<400> 12
 gcgcggtacc tgataaaagg agagggtaaa gag 33

<210> 13
 <211> 1140
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (1) .. (1140)

<400> 13
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 Met Met Arg Lys Lys Ser Phe Trp Leu Gly Met Leu Thr Ala Leu Met
 1 5 10 15
 ctc gtg ttc acg atg gcc ttc agc gat tcc gcg tct gct gct cag ccg 96
 Leu Val Phe Thr Met Ala Phe Ser Asp Ser Ala Ser Ala Ala Gln Pro
 20 25 30
 gcg aaa aat gtt gaa aag gat tat att gtc gga ttt aag tcg gga gtg 144
 Ala Lys Asn Val Glu Lys Asp Tyr Ile Val Gly Phe Lys Ser Gly Val
 35 40 45
 aaa acc gca tcc gtc aaa aag gac atc atc aaa gag agc ggc gga aaa 192
 Lys Thr Ala Ser Val Lys Lys Asp Ile Ile Lys Glu Ser Gly Gly Lys
 50 55 60

gtg	gac	aag	cag	ttt	aga	atc	atc	aac	gcg	gca	aaa	gcg	aag	cta	gac	240
Val	Asp	Lys	Gln	Phe	Arg	Ile	Ile	Asn	Ala	Ala	Lys	Ala	Lys	Leu	Asp	
65					70				75						80	
aaa	gaa	gcg	ctt	gag	gaa	gtc	aaa	aat	gat	ccg	gat	gtc	gct	tat	gtg	288
Lys	Glu	Ala	Leu	Glu	Glu	Val	Lys	Asn	Asp	Pro	Asp	Val	Ala	Tyr	Val	
				85					90					95		
gaa	gag	gat	cac	gta	gct	cat	gct	ttg	gcg	caa	acc	gtt	cct	tac	ggc	336
Glu	Glu	Asp	His	Val	Ala	His	Ala	Leu	Ala	Gln	Thr	Val	Pro	Tyr	Gly	
			100					105					110			
att	cct	ctc	att	aaa	gcg	gac	aaa	gtg	cag	gct	caa	ggc	tac	aag	gga	384
Ile	Pro	Leu	Ile	Lys	Ala	Asp	Lys	Val	Gln	Ala	Gln	Gly	Tyr	Lys	Gly	
		115					120					125				
gcg	aac	gta	aaa	gtc	gcc	gtc	ctg	gat	aca	gga	atc	caa	gct	tct	cat	432
Ala	Asn	Val	Lys	Val	Ala	Val	Leu	Asp	Thr	Gly	Ile	Gln	Ala	Ser	His	
	130					135					140					
ccg	gac	ttg	aac	gta	gtc	ggc	gga	gca	agc	ttc	gta	gct	ggc	gaa	gct	480
Pro	Asp	Leu	Asn	Val	Val	Gly	Gly	Ala	Ser	Phe	Val	Ala	Gly	Glu	Ala	
145					150				155					160		
tat	aac	acc	gac	ggc	aac	gga	cac	ggc	acg	cat	gtt	gcc	ggc	aca	gta	528
Tyr	Asn	Thr	Asp	Gly	Asn	Gly	His	Gly	Thr	His	Val	Ala	Gly	Thr	Val	
				165				170						175		
gct	gcg	ctt	gac	aat	aca	acg	ggt	gta	tta	ggc	gtt	gcg	ccg	aac	gta	576
Ala	Ala	Leu	Asp	Asn	Thr	Thr	Gly	Val	Leu	Gly	Val	Ala	Pro	Asn	Val	
			180					185					190			
tcc	ttg	tac	gcg	gtt	aaa	gtg	ctg	aat	tca	agc	gga	agc	gga	tct	tac	624
Ser	Leu	Tyr	Ala	Val	Lys	Val	Leu	Asn	Ser	Ser	Gly	Ser	Gly	Ser	Tyr	
		195					200					205				
agc	ggc	att	gta	agc	gga	atc	gag	tgg	gcg	acg	aca	aac	ggc	atg	gat	672
Ser	Gly	Ile	Val	Ser	Gly	Ile	Glu	Trp	Ala	Thr	Thr	Asn	Gly	Met	Asp	
	210					215					220					
gtt	atc	aac	atg	agc	ctt	gga	gga	cca	tca	ggc	tca	aca	gcg	atg	aaa	720
Val	Ile	Asn	Met	Ser	Leu	Gly	Gly	Pro	Ser	Gly	Ser	Thr	Ala	Met	Lys	
225					230					235				240		
cag	gcg	gtt	gac	aat	gca	tat	gca	aga	ggg	gtt	gtc	gtt	gtg	gcg	gct	768
Gln	Ala	Val	Asp	Asn	Ala	Tyr	Ala	Arg	Gly	Val	Val	Val	Val	Ala	Ala	
				245				250						255		
gct	ggg	aac	agc	gga	tct	tca	gga	aac	acg	aat	aca	atc	ggc	tat	cct	816
Ala	Gly	Asn	Ser	Gly	Ser	Ser	Gly	Asn	Thr	Asn	Thr	Ile	Gly	Tyr	Pro	
			260				265						270			
gcg	aaa	tac	gac	tct	gtc	atc	gca	gtt	ggc	gcg	gta	gac	cct	aac	agc	864
Ala	Lys	Tyr	Asp	Ser	Val	Ile	Ala	Val	Gly	Ala	Val	Asp	Pro	Asn	Ser	
		275					280					285				
aac	aga	gct	tca	ttt	tcc	agc	gtc	gga	gca	gag	ctt	gaa	gtc	atg	gct	912
Asn	Arg	Ala	Ser	Phe	Ser	Ser	Val	Gly	Ala	Glu	Leu	Glu	Val	Met	Ala	
	290					295					300					
cct	ggc	gca	ggc	gtg	tac	agc	act	tac	cca	acc	agc	act	tat	gca	aca	960
Pro	Gly	Ala	Gly	Val	Tyr	Ser	Thr	Tyr	Pro	Thr	Ser	Thr	Tyr	Ala	Thr	
305					310					315				320		
ttg	aac	gga	acg	tca	atg	gct	tct	cct	cat	gta	gcg	gga	gca	gca	gct	1008
Leu	Asn	Gly	Thr	Ser	Met	Ala	Ser	Pro	His	Val	Ala	Gly	Ala	Ala	Ala	
				325				330						335		
ttg	atc	ttg	tca	aaa	cat	ccg	aac	ctt	tca	gct	tca	caa	gtc	cgc	aac	1056
Leu	Ile	Leu	Ser	Lys	His	Pro	Asn	Leu	Ser	Ala	Ser	Gln	Val	Arg	Asn	
			340					345					350			
cgt	ctc	tcc	agt	acg	gcg	act	tat	ttg	gga	agc	tcc	ttc	tac	tat	gga	1104
Arg	Leu	Ser	Ser	Thr	Ala	Thr	Tyr	Leu	Gly	Ser	Ser	Phe	Tyr	Tyr	Gly	
		355					360					365				

Ala Gly Asn Ser Gly Ser Ser Gly Asn Thr Asn Thr Ile Gly Tyr Pro
260 265 270

Ala Lys Tyr Asp Ser Val Ile Ala Val Gly Ala Val Asp Pro Asn Ser
275 280 285

Asn Arg Ala Ser Phe Ser Ser Val Gly Ala Glu Leu Glu Val Met Ala
290 295 300

Pro Gly Ala Gly Val Tyr Ser Thr Tyr Pro Thr Ser Thr Tyr Ala Thr
305 310 315 320

Leu Asn Gly Thr Ser Met Ala Ser Pro His Val Ala Gly Ala Ala Ala
325 330 335

Leu Ile Leu Ser Lys His Pro Asn Leu Ser Ala Ser Gln Val Arg Asn
340 345 350

Arg Leu Ser Ser Thr Ala Thr Tyr Leu Gly Ser Ser Phe Tyr Tyr Gly
355 360 365

Lys Gly Leu Ile Asn Val Glu Ala Ala Ala Gln
370 375

<210> 15
<211> 1146
<212> DNA
<213> Bacillus subtilis

<220>
<221> CDS
<222> (1)..(1146)

<400> 15
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Val Arg Ser Lys Lys Leu Trp Ile Ser Leu Leu Phe Ala Leu Thr Leu
1 5 10 15
atc ttt acg atg gcg ttc agc aac atg tct gcg cag gct gcc gga aaa 96
Ile Phe Thr Met Ala Phe Ser Asn Met Ser Ala Gln Ala Ala Gly Lys
20 25 30
agc agt aca gaa aag aaa tac att gtc gga ttt aaa cag aca atg agt 144
Ser Ser Thr Glu Lys Lys Tyr Ile Val Gly Phe Lys Gln Thr Met Ser
35 40 45
gcc atg agt tcc gcc aag aaa aag gat gtt att tct gaa aaa ggc gga 192
Ala Met Ser Ser Ala Lys Lys Lys Asp Val Ile Ser Glu Lys Gly Gly
50 55 60
aag gtt caa aag caa ttt aag tat gtt aac gcg gcc gca gca aca ttg 240
Lys Val Gln Lys Gln Phe Lys Tyr Val Asn Ala Ala Ala Ala Thr Leu
65 70 75 80
gat gaa aaa gct gta aaa gaa ttg aaa aaa gat ccg agc gtt gca tat 288
Asp Glu Lys Ala Val Lys Glu Leu Lys Lys Asp Pro Ser Val Ala Tyr
85 90 95
gtg gaa gaa gat cat att gca cat gaa tat gcg caa tct gtt cct tat 336
Val Glu Glu Asp His Ile Ala His Glu Tyr Ala Gln Ser Val Pro Tyr
100 105 110
ggc att tct caa att aaa gcg ccg gct ctt cac tct caa ggc tac aca 384
Gly Ile Ser Gln Ile Lys Ala Pro Ala Leu His Ser Gln Gly Tyr Thr
115 120 125

ggc tct aac gta aaa gta gct gtt atc gac agc gga att gac tct tct	432
Gly Ser Asn Val Lys Val Ala Val Ile Asp Ser Gly Ile Asp Ser Ser	
130 135 140	
cat cct gac tta aac gtc aga ggc gga gca agc ttc gta cct tct gaa	480
His Pro Asp Leu Asn Val Arg Gly Gly Ala Ser Phe Val Pro Ser Glu	
145 150 155 160	
aca aac cca tac cag gac ggc agt tct cac ggt acg cat gta gcc ggt	528
Thr Asn Pro Tyr Gln Asp Gly Ser Ser His Gly Thr His Val Ala Gly	
165 170 175	
acg att gcc gct ctt aat aac tca atc ggt gtt ctg ggc gta gcg cca	576
Thr Ile Ala Ala Leu Asn Asn Ser Ile Gly Val Leu Gly Val Ala Pro	
180 185 190	
agc gca tca tta tat gca gta aaa gtg ctt gat tca aca gga agc ggc	624
Ser Ala Ser Leu Tyr Ala Val Lys Val Leu Asp Ser Thr Gly Ser Gly	
195 200 205	
caa tat agc tgg att att aac ggc att gag tgg gcc att tcc aac aat	672
Gln Tyr Ser Trp Ile Ile Asn Gly Ile Glu Trp Ala Ile Ser Asn Asn	
210 215 220	
atg gat gtt atc aac atg agc ctt ggc gga cct act ggt tct aca gcg	720
Met Asp Val Ile Asn Met Ser Leu Gly Gly Pro Thr Gly Ser Thr Ala	
225 230 235 240	
ctg aaa aca gtc gtt gac aaa gcc gtt tcc agc ggt atc gtc gtt gct	768
Leu Lys Thr Val Val Asp Lys Ala Val Ser Ser Gly Ile Val Val Ala	
245 250 255	
gcc gca gcc gga aac gaa ggt tca tcc gga agc aca agc aca gtc ggc	816
Ala Ala Ala Gly Asn Glu Gly Ser Ser Gly Ser Thr Ser Thr Val Gly	
260 265 270	
tac cct gca aaa tat cct tct act att gca gta ggt gcg gta aac agc	864
Tyr Pro Ala Lys Tyr Pro Ser Thr Ile Ala Val Gly Ala Val Asn Ser	
275 280 285	
agc aac caa aga gct tca ttc tcc agc gca ggt tct gag ctt gat gtg	912
Ser Asn Gln Arg Ala Ser Phe Ser Ser Ala Gly Ser Glu Leu Asp Val	
290 295 300	
atg gct cct ggc gtg tcc atc caa agc aca ctt cct gga ggc act tac	960
Met Ala Pro Gly Val Ser Ile Gln Ser Thr Leu Pro Gly Gly Thr Tyr	
305 310 315 320	
ggc gct tat aac gga acg tcc atg gcg act cct cac gtt gcc cga gca	1008
Gly Ala Tyr Asn Gly Thr Ser Met Ala Thr Pro His Val Ala Arg Ala	
325 330 335	
gca gcg tta att ctt tct aag cac ccg act tgg aca aac gcg caa gtc	1056
Ala Ala Leu Ile Leu Ser Lys His Pro Thr Trp Thr Asn Ala Gln Val	
340 345 350	
cgt gat cgt tta gaa agc act gca aca tat ctt gga aac tct ttc tac	1104
Arg Asp Arg Leu Glu Ser Thr Ala Thr Tyr Leu Gly Asn Ser Phe Tyr	
355 360 365	
tat gga aaa ggg tta atc aac gta caa gca gct gca caa taa	1146
Tyr Gly Lys Gly Leu Ile Asn Val Gln Ala Ala Gln	
370 375 380	

<210> 16
 <211> 381
 <212> PRT
 <213> Bacillus subtilis

<400> 16
 Val Arg Ser Lys Lys Leu Trp Ile Ser Leu Leu Phe Ala Leu Thr Leu
 1 5 10 15

Ile	Phe	Thr	Met	Ala	Phe	Ser	Asn	Met	Ser	Ala	Gln	Ala	Ala	Gly	Lys	
			20					25					30			
Ser	Ser	Thr	Glu	Lys	Lys	Tyr	Ile	Val	Gly	Phe	Lys	Gln	Thr	Met	Ser	
		35					40					45				
Ala	Met	Ser	Ser	Ala	Lys	Lys	Lys	Asp	Val	Ile	Ser	Glu	Lys	Gly	Gly	
	50					55					60					
Lys	Val	Gln	Lys	Gln	Phe	Lys	Tyr	Val	Asn	Ala	Ala	Ala	Ala	Thr	Leu	
65					70				75						80	
Asp	Glu	Lys	Ala	Val	Lys	Glu	Leu	Lys	Lys	Asp	Pro	Ser	Val	Ala	Tyr	
				85				90						95		
Val	Glu	Glu	Asp	His	Ile	Ala	His	Glu	Tyr	Ala	Gln	Ser	Val	Pro	Tyr	
			100					105					110			
Gly	Ile	Ser	Gln	Ile	Lys	Ala	Pro	Ala	Leu	His	Ser	Gln	Gly	Tyr	Thr	
		115					120					125				
Gly	Ser	Asn	Val	Lys	Val	Ala	Val	Ile	Asp	Ser	Gly	Ile	Asp	Ser	Ser	
	130					135					140					
His	Pro	Asp	Leu	Asn	Val	Arg	Gly	Gly	Ala	Ser	Phe	Val	Pro	Ser	Glu	
145					150					155					160	
Thr	Asn	Pro	Tyr	Gln	Asp	Gly	Ser	Ser	His	Gly	Thr	His	Val	Ala	Gly	
				165					170					175		
Thr	Ile	Ala	Ala	Leu	Asn	Asn	Ser	Ile	Gly	Val	Leu	Gly	Val	Ala	Pro	
			180					185					190			
Ser	Ala	Ser	Leu	Tyr	Ala	Val	Lys	Val	Leu	Asp	Ser	Thr	Gly	Ser	Gly	
		195					200					205				
Gln	Tyr	Ser	Trp	Ile	Ile	Asn	Gly	Ile	Glu	Trp	Ala	Ile	Ser	Asn	Asn	
	210					215					220					
Met	Asp	Val	Ile	Asn	Met	Ser	Leu	Gly	Gly	Pro	Thr	Gly	Ser	Thr	Ala	
225					230					235					240	
Leu	Lys	Thr	Val	Val	Asp	Lys	Ala	Val	Ser	Ser	Gly	Ile	Val	Val	Ala	
				245					250					255		
Ala	Ala	Ala	Gly	Asn	Glu	Gly	Ser	Ser	Gly	Ser	Thr	Ser	Thr	Val	Gly	
			260					265					270			
Tyr	Pro	Ala	Lys	Tyr	Pro	Ser	Thr	Ile	Ala	Val	Gly	Ala	Val	Asn	Ser	
		275					280					285				
Ser	Asn	Gln	Arg	Ala	Ser	Phe	Ser	Ser	Ala	Gly	Ser	Glu	Leu	Asp	Val	
	290					295					300					
Met	Ala	Pro	Gly	Val	Ser	Ile	Gln	Ser	Thr	Leu	Pro	Gly	Gly	Thr	Tyr	
305					310					315					320	

Gly Ala Tyr Asn Gly Thr Ser Met Ala Thr Pro His Val Ala Arg Ala
325 330 335

Ala Ala Leu Ile Leu Ser Lys His Pro Thr Trp Thr Asn Ala Gln Val
340 345 350

Arg Asp Arg Leu Glu Ser Thr Ala Thr Tyr Leu Gly Asn Ser Phe Tyr
355 360 365

Tyr Gly Lys Gly Leu Ile Asn Val Gln Ala Ala Ala Gln
370 375 380

<210> 17
<211> 32
<212> DNA
<213> Artificial

<220>
<223> Description of artificial sequence: Primer

<400> 17
ggaagatcta gaggttttca ccgtcatcac cg

32

<210> 18
<211> 34
<212> DNA
<213> Artificial

<220>
<223> Description of artificial sequence: Primer

<400> 18
ggtagatctc tttcgtcgtc ttcaagaatt ccgc

34

<210> 19
<211> 441
<212> DNA
<213> Bacillus subtilis

<220>
<221> CDS
<222> (1)..(441)

<400> 19
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Ile Lys Ala Asp Lys Val Gln Ala Gln Gly Phe Lys Gly Ala Asn Val
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aaa gta gcc gtc ctg gat aca gga atc caa gct tct cat ccg gac ttg
Lys Val Ala Val Leu Asp Thr Gly Ile Gln Ala Ser His Pro Asp Leu
20 25 30
aac gta gtc ggc gga gca agc ttt gtg gct ggc gaa gct tat aac acc
Asn Val Val Gly Gly Ala Ser Phe Val Ala Gly Glu Ala Tyr Asn Thr
35 40 45
gac ggc aac gga cac ggc gca cat gtt gcc ggt aca gta gct gcg ctt
Asp Gly Asn Gly His Gly Ala His Val Ala Gly Thr Val Ala Ala Leu
50 55 60

48

96

144

192

<213> Bacillus subtilis

<220>

<221> CDS

<222> (1)..(576)

<400> 21

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1				5				10						15		
aaa	gta	gcc	gta	att	gac	agc	gga	att	gac	tct	tct	cat	cct	gac	ttg	96
Lys	Val	Ala	Val	Ile	Asp	Ser	Gly	Ile	Asp	Ser	Ser	His	Pro	Asp	Leu	
			20					25					30			
aac	gtc	aga	ggc	gga	gca	agc	ttc	gta	cct	tct	gaa	aca	aac	cca	tac	144
Asn	Val	Arg	Gly	Gly	Ala	Ser	Phe	Val	Pro	Ser	Glu	Thr	Asn	Pro	Tyr	
		35					40					45				
caa	gat	ggc	agt	tct	cac	ggc	aca	cat	gta	gcc	ggt	acg	gtt	gcc	gca	192
Gln	Asp	Gly	Ser	Ser	His	Gly	Thr	His	Val	Ala	Gly	Thr	Val	Ala	Ala	
	50					55					60					
ctt	aat	aac	tca	atc	ggc	gtt	ttg	ggc	gta	gcg	cca	aac	gca	tcg	tta	240
Leu	Asn	Asn	Ser	Ile	Gly	Val	Leu	Gly	Val	Ala	Pro	Asn	Ala	Ser	Leu	
65				70				75					80			
tat	gca	gta	aaa	gtt	ctt	gat	tca	aca	gga	aac	ggc	caa	tac	agc	tgg	288
Tyr	Ala	Val	Lys	Val	Leu	Asp	Ser	Thr	Gly	Asn	Gly	Gln	Tyr	Ser	Trp	
			85					90					95			
att	att	aac	ggc	att	gag	tgg	gcc	att	tcc	aac	aaa	atg	gac	gtg	att	336
Ile	Ile	Asn	Gly	Ile	Glu	Trp	Ala	Ile	Ser	Asn	Lys	Met	Asp	Val	Ile	
		100					105						110			
aac	atg	agc	ctt	ggc	gga	cct	tct	ggt	tct	aca	gct	ttg	aaa	tca	gtc	384
Asn	Met	Ser	Leu	Gly	Gly	Pro	Ser	Gly	Ser	Thr	Ala	Leu	Lys	Ser	Val	
		115				120						125				
gtt	gat	aga	gcc	gta	gcc	agc	ggt	atc	gtc	gtt	gtt	gct	gca	gcc	gga	432
Val	Asp	Arg	Ala	Val	Ala	Ser	Gly	Ile	Val	Val	Val	Ala	Ala	Ala	Gly	
	130					135					140					
aat	gaa	ggc	act	tcc	gga	agc	tca	agc	aca	atc	ggc	tat	cct	gca	aaa	480
Asn	Glu	Gly	Thr	Ser	Gly	Ser	Ser	Ser	Thr	Ile	Gly	Tyr	Pro	Ala	Lys	
145					150					155					160	
tat	cct	tct	acc	att	gcg	gta	ggt	gcg	gta	aac	agc	agc	aac	caa	aga	528
Tyr	Pro	Ser	Thr	Ile	Ala	Val	Gly	Ala	Val	Asn	Ser	Ser	Asn	Gln	Arg	
			165					170						175		
ggt	tca	ttc	tca	agc	gta	ggt	cct	gag	ctt	gaa	gtc	atg	gct	cct	ggc	576
Gly	Ser	Phe	Ser	Ser	Val	Gly	Pro	Glu	Leu	Glu	Val	Met	Ala	Pro	Gly	
			180					185					190			

<210> 22

<211> 192

<212> PRT

<213> Bacillus subtilis

<400> 22

Ile	Lys	Ala	Pro	Ala	Leu	His	Ser	Gln	Gly	Tyr	Thr	Gly	Ser	Asn	Val
1				5				10						15	
Lys	Val	Ala	Val	Ile	Asp	Ser	Gly	Ile	Asp	Ser	Ser	His	Pro	Asp	Leu
			20					25					30		
Asn	Val	Arg	Gly	Gly	Ala	Ser	Phe	Val	Pro	Ser	Glu	Thr	Asn	Pro	Tyr
		35					40					45			

Gln	Asp	Gly	Ser	Ser	His	Gly	Thr	His	Val	Ala	Gly	Thr	Val	Ala	Ala	
50						55					60					
Leu	Asn	Asn	Ser	Ile	Gly	Val	Leu	Gly	Val	Ala	Pro	Asn	Ala	Ser	Leu	
65					70					75					80	
Tyr	Ala	Val	Lys	Val	Leu	Asp	Ser	Thr	Gly	Asn	Gly	Gln	Tyr	Ser	Trp	
				85					90					95		
Ile	Ile	Asn	Gly	Ile	Glu	Trp	Ala	Ile	Ser	Asn	Lys	Met	Asp	Val	Ile	
			100					105					110			
Asn	Met	Ser	Leu	Gly	Gly	Pro	Ser	Gly	Ser	Thr	Ala	Leu	Lys	Ser	Val	
		115					120					125				
Val	Asp	Arg	Ala	Val	Ala	Ser	Gly	Ile	Val	Val	Val	Ala	Ala	Ala	Gly	
	130					135					140					
Asn	Glu	Gly	Thr	Ser	Gly	Ser	Ser	Ser	Thr	Ile	Gly	Tyr	Pro	Ala	Lys	
145					150					155					160	
Tyr	Pro	Ser	Thr	Ile	Ala	Val	Gly	Ala	Val	Asn	Ser	Ser	Asn	Gln	Arg	
				165					170					175		
Gly	Ser	Phe	Ser	Ser	Val	Gly	Pro	Glu	Leu	Glu	Val	Met	Ala	Pro	Gly	
			180					185					190			

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